

Another advantage for cleaning raw sequences early is to prevent poor sequence regions from being considered for probe picking. In the following example sequence segment, a region in which the actual probes (25 base long) would be picked is underlined:

SEQ ID NO: 02 gatcgattccgattccgggttagcctgaccgaaaaaaaaaaaaa

In the Drawings

As indicated by red ink on the attached drawings, please amend the drawings as follows:

Please replace with newly submitted "Figure 7".

REMARKS

In this amendment, specification has been amended to render the application more legible and to correct informalities. Figure 7 has been replaced to add Sequence ID Numbers. Applicant's attorney hereby state that no new matter has been entered.

Respectfully submitted,

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## In the Specification

Please replace which starts on line 3, page 14 with the following:

Cleaning sequences early offers several advantages. Poor quality sequences may interfere with sequence clustering and alignment tools' capability to refine clusters and align assemblies. For example, the following sequence has a high low-complexity region (underlined region):

[illegible]

Please replace which starts on line 9, page 14 with the following:

Another advantage for cleaning raw sequences early is to prevent poor sequence regions from being considered for probe picking. In the following example sequence segment, a region in which the actual probes (25 base long) would be picked is underlined:

SEQ ID NO: 02 gatcgattccgattccgggttagcctgaccgaaaaaaaaaaaaaaaa



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SEQ ID NO: 03

~~Sequence A:~~ AGCTTTGACT.GTTCAAGCATTX

SEQ ID NO: 04

~~Sequence B:~~ TTGACT

SEQ ID NO: 05

~~Sequence C:~~ AGATTTGGCTA

~~Sequence D:~~ AGnnTTGGCTAGTT

SEQ ID NO: 07  
~~Consensus X:~~ AGNTTTGNCTNGTTCAAGCATTN

FIGURE 7